Kyle J Gaulton

List of Publications by Year
in descending order

57	9,622	70961 41	133063 59
papers	citations	h-index	g-index

81	81	81	16661
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
2	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
3	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
4	A map of open chromatin in human pancreatic islets. Nature Genetics, 2010, 42, 255-259.	9.4	515
5	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. Nature Genetics, 2014, 46, 136-143.	9.4	475
6	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	9.4	452
7	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
8	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
9	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. PLoS Medicine, 2018, 15, e1002654.	3.9	373
10	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
11	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
12	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
13	A single-cell atlas of chromatin accessibility in the human genome. Cell, 2021, 184, 5985-6001.e19.	13.5	194
14	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
15	Transcript Expression Data from Human Islets Links Regulatory Signals from Genome-Wide Association Studies for Type 2 Diabetes and Glycemic Traits to Their Downstream Effectors. PLoS Genetics, 2015, 11, e1005694.	1.5	178
16	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. PLoS ONE, 2013, 8, e55272.	1.1	178
17	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. Nature, 2021, 594, 398-402.	13.7	170
18	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158

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19	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
20	Single-cell multiomic profiling of human lungs reveals cell-type-specific and age-dynamic control of SARS-CoV2 host genes. ELife, 2020, 9, .	2.8	129
21	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	1.5	124
22	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
23	Comprehensive Association Study of Type 2 Diabetes and Related Quantitative Traits With 222 Candidate Genes. Diabetes, 2008, 57, 3136-3144.	0.3	104
24	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. ELife, 2018, 7, .	2.8	103
25	Single-cell chromatin accessibility identifies pancreatic islet cell typeâ€“ and state-specific regulatory programs of diabetes risk. Nature Genetics, 2021, 53, 455-466.	9.4	100
26	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
27	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	13.7	95
28	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	13.7	89
29	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
30	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	5.8	82
31	Identification of a Regulatory Variant That Binds FOXA1 and FOXA2 at the CDC123/CAMK1D Type 2 Diabetes GWAS Locus. PLoS Genetics, 2014, 10, e1004633.	1.5	80
32	A computational system to select candidate genes for complex human traits. Bioinformatics, 2007, 23, 1132-1140.	1.8	79
33	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
34	Characterizing cis-regulatory elements using single-cell epigenomics. Nature Reviews Genetics, 2023, 24, 21-43.	7.7	72
35	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
36	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	3.8	65

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37	Cardiac cell typeâ€“specific gene regulatory programs and disease risk association. Science Advances, 2021, 7, .	4.7	63
38	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. American Journal of Human Genetics, 2017, 100, 238-256.	2.6	60
39	Lipid-Induced Epigenomic Changes in Human Macrophages Identify a Coronary Artery Disease-Associated Variant that Regulates PPAP2B Expression through Altered C/EBP-Beta Binding. PLoS Genetics, 2015, 11, e1005061.	1.5	56
40	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	2.6	55
41	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	2.6	49
42	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
43	Shared genetic risk contributes to type 1 and type 2 diabetes etiology. Human Molecular Genetics, 2018, , .	1.4	45
44	The South Asian Genome. PLoS ONE, 2014, 9, e102645.	1.1	43
45	Mechanisms of Type 2 Diabetes Risk Loci. Current Diabetes Reports, 2017, 17, 72.	1.7	39
46	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. Nature Genetics, 2019, 51, 1506-1517.	9.4	35
47	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. Genome Medicine, 2019, 11, 19.	3.6	33
48	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
49	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. Nature Communications, 2021, 12, 6636.	5.8	31
50	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
51	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	2.6	24
52	Mutations and variants of ONECUT1 in diabetes. Nature Medicine, 2021, 27, 1928-1940.	15.2	24
53	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, 2021, 10, .	2.8	15
54	Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. PLoS Genetics, 2021, 17, e1009531.	1.5	13

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55	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	1.4	8
56	Neighborhoods to Nucleotidesâ€"Advances and Gaps for an Obesity Disparities Systems Epidemiology Model. Current Epidemiology Reports, 2019, 6, 476-485.	1.1	1
57	Whole Genome and Exome Sequencing of Type 2 Diabetes. Frontiers in Diabetes, 2014, , 29-41.	0.4	0